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## OM protein - protein search, using sw model

Run on: June 24, 2002, 20:49:16 ; Search time 25.54 Seconds

(without alignments)  
440.277 Million cell updates/sec

Title:	US-09-664-326-23
Perfect score:	368
Sequence:	1 LTYTDCTESQNLCLCEGSN.....PKPQSHNDGDFEEIPEEYLQ 65
Scoring table:	BLOSUM62
Gapext:	0.5
Searched:	562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters:	562222
Minimum DB seq length:	0
Maximum DB seq length:	2000000000
Post-processing:	Minimum Match 0.8 Maximum Match 10.0 Listing first 45 summaries
Database :	SPTREMBL_19;*
1:	sp_archea:*
2:	sp_bacteria:*
3:	sp_fungi:*
4:	sp_human:*
5:	sp_invertebrate:*
6:	sp_mammal:*
7:	sp_mhc:*
8:	sp_organelle:*
9:	sp_phage:*
10:	sp_plant:*
11:	sp_rabbit:*
12:	sp Rodent:*
13:	sp_virus:*
14:	sp_vertebrate:*
15:	sp Unclassified:*
16:	sp_bacterian:*
17:	sp_archeap:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RESULT	1	PRELIMINARY;	PRT:	84 AA.
ID	Q07557			
AC	Q07557;			
DT	01-MOV-1998 (TREMBL); 08, Last sequence update)			
DT	01-NUN-2001 (TREMBL); 17, Last annotation update)			
DE	HIRUDIN HM2 PRECURSOR (SURFRUDIN).			
GN	Hirudinaria manillensis (Buffalo leech).			
OS	Hirudinaria manillensis (Buffalo leech).			
OC	Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;			
OC	Arychobdellida; Hirudiniformes; Hirudinidae; Hirudinaria.			
NCBI-TaxID	6419;			
RN	[1]			
RP	SEQUENCE FROM N.A. AND SEQUENCE OF 21-84.			
RX	Medline=93285156; PubMed=768281;			
RA	Sacchetti E., Nitti G., Valsasina B., Orsini G., Visco C., Ferrera M., Sawyer R.T., Sarmientos P.;			
RA	"Novel hirudin variants from the leech Hirudinaria manillensis. Amino acid sequence, cDNA cloning and genomic organization."			
RT	Eur. J. Biochem. 214:295-304(1993)			
RL	-1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-THROMBIN. THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.			
CC	CC			
CC	CC			
CC	-!- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.			
DR	EMBL: X72286; CAAS51293.; -.			
DR	HSSP: P01050; SHTR.			
DR	InterPro: IPR00429; Hirudin.			
DR	PFam: PF00713; Hirudin; 1.			
DR	PRINTS: PR0077; HIRUDIN.			
DR	ProDom: PD004216; Hirudin; 1.			
KW	Serine protease inhibitor; Multigene family; Signal.			
FT	SIGNAL 1 20			
FT	CHAIN 21 84			
FT	DISUFLID 26 34			
FT	DISUFLID 36 48			
FT	DISUFLID 42 57			
FT	SEQUENCE 84 AA; 9004 MW; CCBAD85ET1B4FF7 CRC64;			

Result No.	Score	Query Match Length	DB ID	Description
1	247	67.1	84	5
2	230	62.5	84	5
3	138	37.5	25	5
4	136	37.0	25	5
5	74.5	20.2	1331	13 Q9W93
6	74	20.1	248	5 096962
7	74	20.1	2352	5 061240
8	71	19.3	608	5 Q9V80
9	70	19.0	323	2 Q93NY8
10	69	18.8	315	13 Q9W600
11	68.5	23.3	5 094711	paramaecium
12	68	18.5	184	2 Q9RB30
13	68	18.5	278	2 Q9XCP8
14	68	18.5	364	2 084968
15	66.5	18.1	516	3 Q96UY3
16	66.5	18.1	645	5 Q9VTR2

Query Match 67.1%; Score 247; DB 5; Length 84;  
 Best Local Similarity 71.0%; Pred. No. 2.9e-33;  
 Matches 44; Conservative 6; Mismatches 10; Indels 2; Gaps 1;

QY 1 LTYTDCTESQNLCLCEGSNVCGQNCILQSDGEKRNQCVTGEGTPKPKPSQTEGDFEEIP 60  
 ::||||| ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 21 VSYTDCTESQNLCLCEGSNVCGQNCILQSDGEKRNQCVTGEGTPKPKPSQTEGDFEEIP 78  
 ::||||| ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 61 EE 62  
 QY 79 DE 80

RESULT 2  
 PRELIMINARY; PRT; 84 AA.  
 ID 007558  
 AC 007558;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DE HIRUDIN HML PRECURSOR.  
 GN HML.  
 OS Hirudinaria manillensis (Buffalo leech).  
 Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudinaria;  
 OX NCBI\_TaxID=6419;  
 RN [1]  
 SEQUENCE FROM N.A., AND SEQUENCE OF 21-84.  
 MEDLINE=93285156; PubMed=768281;  
 RA Scacheri E., Nitti G., Valsasina B., Orsini G., Visco C., Ferrera M.,  
 Sawyer R.T., Sarmiento P.;  
 RT "Novel hirudin variants from the leech Hirudinaria manillensis. Amino acid sequence, cDNA cloning and genomic organization.";  
 RL Eur. J. Biochem. 214: 305-304 (1993).  
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.  
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.  
 EMBL; X72485; CAA51292.1; -.  
 DR HSSP; P01050; SHIR; IPR000429; Hirudin.  
 DR InterPro; IPR000429; Hirudin.  
 DR PRAM; PFE0013; Hirudin; 1.  
 DR PRINTS; PR00777; HIRUDIN.  
 DR PRODOM; PP004216; Hirudin; 1.  
 KW Serine protease inhibitor; Multigene family; Signal.

FT SIGNAL 1 20  
 FT CHAIN 21 84  
 FT DISUFIID 26 34  
 FT DISUFIID 36 48  
 FT DISUFIID 42 57  
 FT SEQUENCE 84 AA; 8934 MW; 3AD737ED/2D4C1D CRC64;

Query Match 62.5%; Score 230; DB 5; Length 84;  
 Best Local Similarity 64.5%; Pred. No. 3.7e-21; Indels 2; Gaps 1;  
 Matches 40; Conservative 8; Mismatches 12; Indels 2; Gaps 1;

QY 1 LTYTDCTESQNLCLCEGSNVCGQNCILQSDGEKRNQCVTGEGTPKPKPSQTEGDFEEIP 60  
 ::||||| ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 21 VSYTDCTESQNLCLCEGSNVCGQNCILQSDGEKRNQCVTGEGTPKPKPSQTEGDFEEIP 78  
 ::||||| ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 61 EE 62  
 QY 79 DE 80

RESULT 4  
 PRELIMINARY; PRT; 25 AA.  
 ID 09TWX4  
 AC 09TWX4;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE HIRUDIN VARIANT HV1-THROMBIN INHIBITOR.  
 RL Hirudinaria manillensis (Buffalo leech).  
 Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudinaria;  
 OX NCBI\_TaxID=6419;  
 RN [1]  
 SEQUENCE.  
 RX MEDLINE=92126909; PubMed=1773002;  
 RA Electricwala A., Sawyer R.R., Jones C.P., Atkinson T.;  
 RT "Isolation of thrombin inhibitor from the leech Hirudinaria manillensis. ";  
 RL Blood Coagul. Fibrinolysis 2:83-89(1991).  
 DR HSSP; P01050; IHC.  
 DR IPR000429; Hirudin.  
 DR InterPro; IPR000429; Hirudin.  
 DR PRINTS; PR00777; HIRUDIN.  
 DR PRODOM; PD004216; Hirudin; 1.  
 SQ SEQUENCE 25 AA; 2596 MW; 5296A69277A9457D CRC64;

Query Match 37.5%; Score 138; DB 5; Length 25;  
 Best Local Similarity 92.0%; Pred. No. 4.4e-10; Indels 0; Gaps 0;  
 Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTYTDCTESQNLCLCEGSNVCGQNCILQSDGEKRNQCVTGEGTPKPKPSQTEGDFEEIP 60  
 ::||||| ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1 VYVTDCTESQNLCLCEGSNVCGQ 25  
 ::||||| ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 61 EE 62  
 QY 79 DE 80

RESULT 5  
 PRELIMINARY; PRT; 1331 AA.  
 ID 090W93  
 AC 090W93;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE XANTINE DEHYDROGENASE.  
 OS Poecilia reticulata (Guppy).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthopterygii; Acanthopterygia; Percomorpha; Atherinomorpha;  
 OC Cyprinodontiformes; Poeciliidae; Poecilia;  
 NCBI\_TAXID=8081;

RN [1]

SEQUENCE FROM N.A.  
 TISSUE=CAUDAL FIN;  
 RA Ben J., Lim T.-M., Chan W.-K., Phang V.P.E.;  
 RT "Molecular cloning of xanthine dehydrogenase gene from guppy (Poecilia  
 reticulata).";  
 RT Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AV034103; AAHK59999.1; -;  
 DR SEQUENCE 1331 AA; 146336 MW; E8EE00AA6D36D126 CRC64;

Query Match 20.2%; Score 74.5; DB 13; Length 1331;  
 Best Local Similarity 32.2%; Pred. No. 1.4; Mismatches 7; Indels 22; Gaps 3;  
 Matches 19; Conservative 7; Mismatches 22; Indels 11; Gaps 3;

QY 2 TYTDCTES-GQNCLCCEG-----SNVCGQGNKCTILGSDGERKNQCVTGEGTPKPQSH 51  
 Db 138 TMDDITQALGGNCRCTGYRPIWDGCRCFCQEGNCN -QANGGADCCLNSEGNTNESEH 194

RESULT 6

098962 PRELIMINARY; PRT; 248 AA.

ID 086962 AC DT

01-MAY-1999 (TREMBrel. 10, Created)  
 01-MAY-1999 (TREMBrel. 10, Last sequence update)  
 01-DEC-2001 (TREMBrel. 19, Last annotation update)

DT DE GN CD63R.

OS Suberites domuncula.  
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetraclitomorpha;  
 OC Hadromedida; Suberitidae; Suberites.  
 OX NCBI\_TAXID=55567;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Mueller W.E.G., Schatton W., Wimmer W., Bohm M., Batel R., Filic Z.;  
 RT "Initiation of an aquaculture of sponges for their sustainable  
 production of biactive metabolites in open systems.";  
 RL Mol. Mar. Biol. Biotechnol. 1:569-579(1999).  
 DR EMBL: YI8100; CAAT7026\_1; -.  
 DR InterPro: IPR0031; Transmembrane\_4  
 Pfam: PF00335; transmembrane4; 1.  
 DR PRINIS; PR00259; TMFOUR.  
 KW Receptor.

SQ SEQUENCE 248 AA; 26701 MW; DB0F8D349A2E06EE CRC64;

RESULT 8

09VU80 ID 09VU80 PRELIMINARY; PRT; 608 AA.

AC DT

01-MAY-2000 (TREMBrel. 13, Created)  
 01-MAY-2000 (TREMBrel. 13, Last sequence update)  
 01-JUN-2001 (TREMBrel. 17, Last annotation update)

DT DE GN CG11089 PROTEIN.

OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Articulata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Hydrodiidae; Drosophilidae; Drosophila.  
 NCBI\_TAXID=7227;

RN [1]

RP SEQUENCE FROM N.A.  
 STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10711132;  
 ID 061240 PRELIMINARY; PRT; 2252 AA.

AC 061240; DT 01-AUG-1998 (TREMBrel. 07, Created)  
 DT 01-AUG-1998 (TREMBrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)

DR HNNOTCH PROTEIN.

RA	Abril J.F., Aqbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Balwani R.M., Basu A., Basrai M.A., Bayraktaroglu L., Beasley E.M., Beeson K.L., Betos P.V., Bernan B.P., Bhandari D., Bochkov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cahile E., Center A., Chandra I., Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z., Lasko P., Lei Y., Levitsky A.T.C., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moskrafi A., Mount S.M., Moy M., Murphy B., Muranyi D., Muny M., Nelson D.L., Nelson D.R., Nelson K., Nusskern D.R., Pacieb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., The genome sequence of <i>Drosophila melanogaster</i> .; RT	RT combinations of immunoreactive recombinant proteins.";
RA	Science 287:2185-2195(2000); RT	RL J. Clin. Microbiol. 39:2466-2476(2001).
RA	EMBL; AE003537; AA498101.; RT	DR EMBL; AF356509; AAK6999; 1.
RA	HSSP; Q16928; IMKP.; RT	FT NON TSR 1
RA	FlyBase; FBgn0036369; CG310089.; RT	SQ SEQUENCE 323 AA; 34533 MW; 51E0646ED4F8FDED CRC64;
DR	InterPro; IPR000340; DS_phosphatase.; RT	Query Match 19.0%; Score 70; DB 2; Length 323;
DR	InterPro; IPR000387; TYR_phosphatase.; RT	Best Local Similarity 29.6%; Pred. No. 1.1; 315 AA.
DR	InterPro; IPR000387; TYR_phosphatase.; RT	Matches 21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;
DR	InterPro; IPR000387; TYR_phosphatase.; RT	AC Q9W600; ID Q9W600; DT 01-NOV-1999 (T_EMBLrel. 12, Created)
DR	InterPro; IPR000387; TYR_phosphatase.; RT	DT 01-NOV-1999 (T_EMBLrel. 12, Last sequence update)
DR	InterPro; IPR000387; TYR_phosphatase.; RT	DT 01-DEC-2001 (T_EMBLrel. 19, Last annotation update)
DR	InterPro; IPR000387; TYR_phosphatase.; RT	DE FLIK PROTEIN.
SQ	SEQUENCE 608 AA; 66963 MW; 71E135E5C7660D1 CRC64; RT	DN FLIK PROTEIN.
RESULT 9	Q93NKB	OS Gallus gallus (Chicken).
ID Q93NKB	~ PRELIMINARY; PRT; 323 AA.	OC Eukaryota; Metazoa; Choristata; Craniata; Vertebrata; Euteleostomi; OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; OC Gallus.
AC 093NKB	Query Match 19.3%; Score 71; DB 5; Length 608; RT	OX NCBI_TaxID=9031;
AC 093NKB	Best Local Similarity 31.0%; Pred. No. 1.6; RT	RP SEQUENCE FROM N.A.
AC 093NKB	Matches 14; Conservative 10; Mismatches 18; Indels 2; Gaps 1; RT	RX MEDLINE=96427308; PubMed=8812133;
QY 11 QNLCLCEGSNWCGQNKCLIGSDGKKNQCVTGEGTPKPSOSHNDG 54	RT Patel K.; Connolly D.; Author H.; Nose K.; RT Cloning and early dorsal-axial expression of Flk, a chick	
Db 199 QNRDICEGN-CSRGKCPKGADQDVGVNGQGEEDEGEG 240	RT follistatin-related gene: Evidence for involvement in RT dorsallisation/neural induction. .";	
Db 199 QNRDICEGN-CSRGKCPKGADQDVGVNGQGEEDEGEG 240	RT Dev. Biol. 178:327-342(1996);	
Db 199 QNRDICEGN-CSRGKCPKGADQDVGVNGQGEEDEGEG 240	RT EMBL; AJ238977; CAB29681; -.	
Db 199 QNRDICEGN-CSRGKCPKGADQDVGVNGQGEEDEGEG 240	RT InterPro; IPR02048; EF-hand.	
Db 199 QNRDICEGN-CSRGKCPKGADQDVGVNGQGEEDEGEG 240	RT InterPro; IPR03645; FOLN.	
Db 199 QNRDICEGN-CSRGKCPKGADQDVGVNGQGEEDEGEG 240	DR pfam; PF00050; kazal; 1.	
Db 199 QNRDICEGN-CSRGKCPKGADQDVGVNGQGEEDEGEG 240	DR SMART; SM00274; FOLN; 1.	
Db 199 QNRDICEGN-CSRGKCPKGADQDVGVNGQGEEDEGEG 240	DR SMART; SM00280; FOLN; 1.	
RR	SEQUENCE FROM N.A.	DR SEQUENCE 315 AA; 35815 MW; C01889E005658A67 CRC64;
RC	STRAIN=WI 1;	DR
RX	MEDLINE=21320744; PubMed=11427556;	RT combinations of immunoreactive recombinant proteins.";
RA	Lodes M.J., Mohamad R., Reynolds L.D., McNeill P., Kolbert C.P., Bruinsma E.S., Benson D.R., Hofmeister E., Reed S.G., Houghton R.L., Persing D.H.;	RL J. Clin. Microbiol. 39:2466-2476(2001).
RA	"Serodiagnosis of human granulocytic ehrlichiosis by using novel	DR EMBL; AF356509; AAK6999; 1.

DT	01-FEB-1997	(TREMBLrel. 02, Last sequence update)	AC	Q9XCP8;
DT	01-FEB-2001	(TREMBLrel. 19, Last annotation update)	DT	01-NOV-1999 (TREMBLrel. 12, Created)
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE	44	KDA MAJOR OUTER MEMBRANE PROTEIN (FRAGMENT).	DE	44 KDA MAJOR OUTER MEMBRANE PROTEIN (FRAGMENT).
OC		Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;	GN	P4-15.
OC		Paramecium; NCBI_TaxID=5888;	OS	Enrichia phagocytophila.
RN	[1]	SEQUENCE FROM N.A.	OC	Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
RX		Medline=92106337; PubMed=1762150;	OC	Rickettsiaceae; Enrichiae; Anaplasma.
RA		Nielson E., You Y., Forney J.; "Cysteine residue periodicity is a conserved structural feature of variable surface proteins from Paramecium tetraurelia."; J. Mol. Biol. 222:835-841(1991).	NCBI_TaxID=948;	RN
RT		DR InterPro; IPR002895; Paramecium_SA.	[1]	SEQUENCE FROM N.A.
RT		DR Pfam; PF01508; Paramecium_SA; 25; SEQUENCE 223 AA; 237078 MW; C064FEDAF7BH873B CRC64;	RC	STRAIN=FZ;
RA		DR InterPro; IPR002566; Surface_Ag_msp4.	RX	Medline=99292751; Pubmed=10364227;
RL		DR Pfam; PF01617; Surface_Ag_2; 1.	RA	Zhi N., Ohashi N., Rikitisa Y.;
EMBL		DR "Multiple p44 genes encoding major outer membrane proteins are expressed in the human granulocytic enrichiosis agent."; DR J. Biol. Chem. 24:17838-17836(1999).	RT	"Multiple p44 genes encoding major outer membrane proteins are expressed in the human granulocytic enrichiosis agent.";
DR		DR EML; AFL135256; AAD14180.1; -.	RL	J. Biol. Chem. 24:17838-17836(1999).
DR		DR InterPro; IPR002566; Surface_Ag_msp4.	DR	InterPro; IPR002566; Surface_Ag_msp4.
DR		DR Pfam; PF01617; Surface_Ag_2; 1.	FT	NON_TER 1 1
SQ		SEQUENCE 278 AA; 23389 MW; BD5E539BB3AB16C7 CRC64;	SQ	SEQUENCE 278 AA; 23389 MW; BD5E539BB3AB16C7 CRC64;
Query Match	18.6%	Score 68.5; DB 5; Length 2233;	Query Match	18.5%; Score 68; DB 2; Length 278;
Best Local Similarity	39.5%	Pred. No. 14; Mismatches	Best Local Similarity	29.6%; Pred. No. 1.6; Mismatches
Matches	17;	Conservative 4; Indels 13; Gaps 9; Gaps 3;	Matches	21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;
QY	6	CTESGQNLCCEGSNVCGQGN--KCILGSDGEK-N-QCVVGEGTPRQSHNDGF-- 45	QY	6 CTESGQNLCCEGSNVCGQGN--KCILGSDGEK-N-QCVVGEGTPRQSHNDGF-- 56
Db	1830	CTTBQQ--CGITRQCGKVNNGCUTGTDGE--CITWAT 1866	Db	120 CGINGSSITNSGANVSETGQVRDFIRATLKEDGSKKNWPTSSGGTPKPVTNDNAKAVA 179
RESULT	12		QY	57 ----EEIPPE 62
ID	Q9RB30	PRELIMINARY; PRT; 184 AA.	Db	180 KDLVQELTPEE 190
AC	Q9RB30;		RESULT	14
DT	01-MAY-2000	(TREMBLrel. 13, created)	ID	084968
DT	01-MAY-2000	(TREMBLrel. 13, last sequence update)	AC	084968;
DT	01-DEC-2001	(TREMBLrel. 19, last annotation update)	DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE	44	KDA MAJOR OUTER MEMBRANE PROTEIN (FRAGMENT).	DT	01-NOV-1998 (TREMBLrel. 08, Created)
GN	P44-15.		DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
OS		Ehrlichia phagocytophila; alpha subdivision; Rickettsiales;	GN	MSP-2C.
OC		Rickettsiaceae; Enrichiae; Anaplasma.	OS	Enrichia phagocytophila.
RC		NCBI_TaxID=948;	OC	Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
RN	[1]	SEQUENCE FROM N.A.	OC	Rickettsiaceae; Enrichiae; Anaplasma.
RP		STRAIN=FZ;	OX	NCBI_TaxID=948;
RX		Medline=99292751; PubMed=10364227;	RN	[1]
RA		Zhi N., Ohashi N., Rikitisa Y.;	RP	SEQUENCE FROM N.A.
RT		"Multi p44 genes encoding major outer membrane proteins are expressed in the human granulocytic ehrlichiosis agent.";	RC	STRAIN=USG3;
RT		J. Biol. Chem. 274:17828-17836(1999).	RX	Medline=9839872; PubMed=9673253;
DR		EMBL; AFL135261; AAD14185.1; -.	RA	Murphy C.I., Storey J.R., Recchia J., Doros-Richert L.A.,
DR		NON_TER 1	RA	Gingrich-Baker C., Monroe K., Barken J.S., Coughlin R.T., Beltz G.A.;
FT		184	RT	"Major antigenic proteins of the agent of human granulocytic ehrlichiosis are encoded by members of a multigene family.";
FT		SEQUENCE 184 AA; 19245 MW; B2C9AD4775FD55A1 CRC64;	RL	Infect. Immun. 66:3711-3718(1998).
SQ			DR	EMBL; AFL02923; AAC3109.1; -.
QY	57	----EEIPPE 62	DR	InterPro; IPR002566; Surface_Ag_msp4.
Db	137	KDLVQELTPEE 147	DR	Pfam; PF01617; Surface_Ag_2; 1.
RESULT	13		SQ	SEQUENCE 364 AA; 38806 MW; 32DA9B830A6153F2 CRC64;
QY	6	CTESQNLCEGSNVCGQGN--KCILGSDGEK-N-QCVVGEGTPRQSHNDGF-- 56	Query Match	18.5%; Score 68; DB 2; Length 364;
Db	77	CGDNGSSTTNSGAVNETQVFRDFIRATLKEDGSKKNWPTSSGGTPKPVTNDNAKAVA 136	Best Local Similarity	29.6%; Pred. No. 2.2; Mismatches
QY	57	----EEIPPE 62	Matches	21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;
Db	137	KDLVQELTPEE 147	QY	6 CTESGQNLCCEGSNVCGQGN--KCILGSDGEK-N-QCVVGEGTPRQSHNDGF-- 56
QY	6	CTESQNLCEGSNVCGQGN--KCILGSDGEK-N-QCVVGEGTPRQSHNDGF-- 56	Db	226 CGDNGSSTTNSGAVNETQVFRDFIRATLKEDGSKKNWPTSSGGTPKPVTNDNAKAVA 285

QY 57 - - - EELIPEE 62  
Db 286 KDLVQELTPEE 296

Q96U3

ID Q96UY3 PRELIMINARY; PRT; 516 AA.  
AC Q96UY3.

DT 01-DEC-2001 (TREMBLER. 19, Created)  
DT 01-DEC-2001 (TREMBLER. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLER. 19, Last annotation update)  
DT 01-DEC-2001 (TREMBLER. 19, Last annotation update)

OS Saccharomyces sp. DH1-1A.  
OC Eukarya; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

NCBI\_TaxID=173900; Saccharomyces; Saccharomyces cerevisiae; RN

RP  
SEQUENCE FROM N.A.  
RC  
STRAIN=DH1-1A;

RX  
RA  
MEDLINE=21486811; F  
Gimble F.S.;

RT "Degeneration of a homing endonuclease wild yeast strain." RT

RL  
NUCLEIC ACIDS Res. 29:4215-4223(2001).  
DR AF389405; AAL18609.1; -.  
EMBL: FT  
NON\_TER 1  
NON\_TER 1  
FT  
NON\_TER 516  
NON\_TER 516

SQ SEQUENCE 51b AA; 5/b644 MW; B41C8024561DC862 CRC64;

Quality	Match	18.1%	Score	0.65	DB	3;	Length	516;
BEST	Local Similarity	25.3%	Pred.	No. 4.9;				
Matches	19;	Conservative	25.3%	Mismatches	28;	Indels	15;	Gaps

24 LINING ENGINEERS LTD

Db 83 QHRAHKSDSSREMPE 97

Search completed: June 24, 2002, 20:51:49  
Job time: 153 sec